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eQTL analysis from microarray data of fibre expressed genes in an inter-specific *Gossypium hirsutum* x *G. barbadense* RIL population.

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Microarrays provide a wealth of genome-wide gene expression data to characterise the biological variability between different plant genotypes, however it remains difficult to link such genomic results to a functional interpretation of how specific gene action determines a particular plant phenotype. Phenotypes themselves can be associated with specific regions of the genome by traditional QTL mapping, but most QTLs are very large physical regions that do not often allow the identification of specific underlying genes, particularly in species like cotton lacking a full genome sequence. Combining QTL and microarray analyses is a novel way to narrow down on subsets of candidate genes whose level of expression can be statistically correlated to regions of the genome, so-called eQTLs, and further correlated to specific phenotypes.

In this study we used a RIL population of 145 lines from an inter-specific cross between a *G. barbadense* Sea-Island accession (VH8) with very high fibre quality and a *G. hirsutum* cultivar of moderate fibre quality (Guazuncho II). The RIL population had been phenotyped for fibre quality traits at multiple sites and in most cases over multiple years and had also been genotyped. The consensus genetic map for the population contained over 600 SSR and AFLP markers and was used as the framework for both phenotypic QTL and eQTL mapping. Microarray analyses (approx. 24,000 genes per array) were carried out on 10 dpa fibre cDNA on 102 of the RILs and the individual gene expression values for each transcript treated as a quantitative trait and mapped to the genome. The distribution of eQTLs was not uniform across the chromosomes, with chromosomes 5 and 12 having more eQTLs than any others. A number eQTL hotspots were identified that may represent the locations of master regulators of fibre expressed genes. A selection of genes co-located with the phenotypic QTLs for fibre traits were also identified and validated by quantitative PCR. Some, but not all eQTLs identified from the microarray data were confirmed by Q-PCR. Large correlations tables of the expression of all the genes on the arrays and specific fibre traits like length, strength and fineness were developed and are also being used to identify potential candidate genes that may be causal in conferring the commercially useful properties of cotton fibres.

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